

SEQUENCE LISTING

<110> KUFER, Peter
 RAUM, Tobias
 BORSCHERT, Katrin
 ZETTL, Florian
 LUTTERBUSE, Ralf



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TECH CENTER 1600/2900

<120> A NOVEL METHOD OF IDENTIFYING BINDING SITE DOMAINS THAT RETAIN THE CAPACITY OF BINDING TO AN EPITOPE

<130> 0147-0199P

<140> US 09/554,465

<141> 2000-10-19

<160> 77

<170> PatentIn version 3.1

<210> 1

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for human costimulatory protein CD80

<400> 1

gcaga~~ttt~~ca ccatgggcc a cacacggagg cag

33

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tggccggag ttatcaggaa aatgctcttg ctgg

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<212> DNA

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<223> primer for human CD80-M79scFv

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agggtacac tccgatatcm arctgcagsa gtcwgg

36

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ctggtaagc ctggggcttc agtgaagatt tcctgc 96

<210> 7
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<220>
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<210> 8
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<223> primer for single-chain Fv fragment (scFv) of the murine anti 17-1A antibody M74 V(H)

<400> 8
tccgatatcm arctgcagsa gtcwggacct gagctggtga agcctggggc ttcagtgaag 60
atttcctgc 69

<210> 9
<211> 64
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<400> 9
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ccag 64

<210> 10
<211> 54
<212> DNA
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<400> 10
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<210> 11
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<400> 11
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<212> DNA
<213> Artificial Sequence

<220>
<223> primer for V(H) chain of human anti-17-1A antibody

<400> 12
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<210> 13
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for V(H) chain of human anti-17-1A antibody

<400> 13
ctgaggagac ggtgacc 17

<210> 14
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for V(L) chain of human anti-17-1A antibody

<400> 14
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<210> 15
<211> 33
<212> DNA
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<223> primer for V(L) chain of human anti-17-1A antibody

<400> 15
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<210> 16
<211> 24
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<223> oligomer encoding six HIS residues

<400> 16
ctagccatca ccatcaccat caca 24

<210> 17
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer encoding six HIS residues

<400> 17
ctagtgtat ggtgtatggat atgg 24

<210> 18
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide for multiple cloning site containing SacI and Xho I overhang

<400> 18
gcagctggtc gacaaatccg gaggtggatggatccgaggtg cagctgc 47

<210> 19
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide for multiple cloning site containing SacI and Xho I overhang

<400> 19
tcgagcagct gcacacctcgga tccaccacccat ccggattttgt cgaccagctg cagct 55

<210> 20
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide containing multiple cloning sites

<400> 20
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ggtaggttctg agctcggtt 79

<210> 21
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide containing multiple cloning sites

<400> 21
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gaggagacgg tgaccgggg 79

<210> 22
<211> 29
<212> DNA
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<220>
<223> primer for M13 gene III domain N2

<400> 22
ggtgtcgaca ctaaacctcc tgagtagcg 29

<210> 23
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for the M13 gene III domain N2

<400> 23
gcctccggaa gcattgacag gaggttgagg 30

<210> 24
<211> 33
<212> DNA
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<220>
<223> primer for detection of positive clones

<400> 24
gcagaattca ccatgggcca cacacggagg cag 33

<210> 25
<211> 39
<212> DNA
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<220>
<223> primer for detection of positive clones

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<210> 26
<211> 32

<212> DNA
<213> Artificial Sequence

<220>
<223> primer for the extracellular region of the human CD54 antigen known as ICAM-1

<400> 26
ctcgaattca ctatggctcc cagcagcccc cg 32

<210> 27
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for the extracellular region of the human CD54 antigen known as ICAM-1

<400> 27
gattccggac tcataccggg gggagagcac 30

<210> 28
<211> 30
<212> DNA
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<220>
<223> primer for the extracellular region of human CD58

<400> 28
aatctagaac catggttgct gggagcgacg 30

<210> 29
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for the extracellular region of human CD58

<400> 29
aagtccggat ctgtgtcttg aatgaccgct gc 32

<210> 30
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for the extracellular region of human CD86 costimulatory protein

<400> 30
aagtctagaa aatggatccc cagtgcacta tg 32

<210> 31
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for the extracellular region of human CD86 costimulatory protein

<400> 31
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<210> 32
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<220>
<223> primers for murine V heavy chain

<400> 32
saggtgcagc tcgaggagtc aggacct 27

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<220>
<223> primers for murine V heavy chain

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<210> 34
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<220>
<223> primers for murine V heavy chain

<400> 34
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<210> 35
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<220>
<223> primers for murine V heavy chain

<400> 35
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<210> 36
<211> 27
<212> DNA
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<220>
<223> primers for murine V heavy chain

<400> 36
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<210> 37
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<212> DNA
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<220>
<223> primers for murine V heavy chain

<400> 37
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<210> 38
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<220>
<223> primers for murine V heavy chain

<400> 38
gaagtgaagc tcgaggagtc tggggga 27

<210> 39
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<220>
<223> primers for murine V heavy chain

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gaggttcagc tcgagcagtc tggagct 27

<210> 40

<211> 34
<212> DNA
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<210> 41
<211> 32
<212> DNA
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<220>
<223> primer for murine V kappa chain

<400> 41
ccagttccga gctcgttg actcaggaat ct 32

<210> 42
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for murine V kappa chain

<400> 42
ccagttccga gctcgttg acgcagccgc cc 32

<210> 43
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for murine V kappa chain

<400> 43
ccagttccga gctcgtgctc acccagtctc ca 32

<210> 44
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for murine V kappa chain

<400> 44
ccagttccga gctccagatg acccagtctc ca 32

<210> 45
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for murine V kappa chain

<400> 45
ccagatgtga gctcgtgatg acccagactc ca 32

<210> 46
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for murine V kappa chain

<400> 46
ccagatgtga gctcgtcatg acccagtctc ca 32

<210> 47
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for murine V kappa chain

<400> 47
ccagttccga gctcgtgatg acacagtctc ca 32

<210> 48
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for murine V kappa chain

<400> 48
tggtgacta gtcgtacgtt tgatctcaag cttggtccc 39

<210> 49
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide for the multiple cloning site

<400> 49
ctagaattct tcgaatccgg aggtgggtgga tccgatatcc cccggcatca tcaccatcat 60
catggag 67

<210> 50
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of double-stranded oligonucleotide designated ACCGS1BAM

<400> 50
ccggagggtgg tggttccggg ggtggaggtt caggcggtgg tg 42

<210> 51
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of double-stranded oligonucleotide designated ACCGS15BAM

<400> 51
gatccaccac cgcctgaacc tccaccccccgaaccaccac ct 42

<210> 52
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide encoded by synthetic oligonucleotide

<400> 52

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
1 5 10

<210> 53
<211> 381
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(381)
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<400> 53

gag gtg cag ctg ctc gag tct ggg gga ggc gtg gtc cag cct ggg agg 48
Glu Val Gln Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc tat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

gca gtt ata tca tat gat gga agt aat aaa tac tat gca gac tcc gtg 192
Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

ctg caa atg aac acg ctg aga gct gag gac acg gct gtg tat tac tgt 288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg aaa gat atg ggg tgg ggc agt ggc tgg aga ccc tac tac tac tac 336
Ala Lys Asp Met Gly Trp Gly Ser Gly Trp Arg Pro Tyr Tyr Tyr Tyr
100 105 110

ggt atg gac gtc tgg ggc caa ggg acc acg gtc acc gtc tcc tca 381
Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 54
<211> 127
<212> PRT
<213> Homo sapiens

<400> 54

Glu Val Gln Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Met Gly Trp Gly Ser Gly Trp Arg Pro Tyr Tyr Tyr Tyr
 100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 55
 <211> 321
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(321)
 <223>

<400> 55
 gag ctc cag atg acc cag tct cca tcc tcc ctg tct gct tct gtg gga 48
 Glu Leu Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 gac aga gtc acc atc act tgt cgg aca agt cag agc att agc agc tat 96
 Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Ser Ser Tyr
 20 25 30
 tta aat tgg tat cag cag aaa cca gga cag cct cct aag ctg ctc att 144
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 35 40 45
 tac tgg gca tct acc cgg gaa tcc ggg gtc cct gac cga ttc agt ggc 192
 Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
 50 55 60
 agc ggg tct ggg aca gat ttc act ctc acc atc agc agt cta caa cct 240
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 gaa gat tct gca act tac tac tgt cag cag agt tac gac atc ccg tac 288
 Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asp Ile Pro Tyr
 85 90 95
 act ttt ggc cag ggg acc aag ctg gag atc aaa 321
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 56

<211> 107
<212> PRT
<213> Homo sapiens

<400> 56

Glu Leu Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
35 40 45

Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asp Ile Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 57
<211> 201
<212> DNA
<213> Artificial Sequence

<220>

<223> sequence designated L-F-NS3Frame (Figure 3.4)

<400> 57
ccgctctaga attccaccat gggatggagc tgcatacatcc tcttcttggc agcaacagct 60
acagggtgtcc actccgacta caaagatgat gacgataagg atatcttcgg aggtgggtgg 120
agcgctattc catatggacg tcccgctcga ggtcgccat catcaccatc atcactgagc 180
ggccgctcta gagtcgaccc c 201

<210> 58
<211> 526
<212> DNA
<213> Artificial Sequence

<220>

<223> M13-Phage and artificial sequence of the MCS

<220>

<221> CDS

<222> (19) .. (429)

<223>

<400> 58

gagctgcagc tggtcgac act aaa cct cct gag tac ggt gat aca cct att 51
Thr Lys Pro Pro Glu Tyr Gly Asp Thr Pro Ile
1 5 10

ccg ggc tat act tat atc aac cct ctc gac ggc act tat ccg cct ggt 99
Pro Gly Tyr Thr Tyr Ile Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly
15 20 25

act gag caa aac ccc gct aat cct aat cct tct ctt gag gag tct cag 147
Thr Glu Gln Asn Pro Ala Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln
30 35 40

cct ctt aat act ttc atg ttt cag aat aat agg ttc cga aat agg cag 195
Pro Leu Asn Thr Phe Met Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln
45 50 55

ggg gca tta act gtt tat acg ggc act gtt act caa ggc act gac ccc 243
Gly Ala Leu Thr Val Tyr Thr Gly Thr Val Thr Gln Gly Thr Asp Pro
60 65 70 75

gtt aaa act tat tac cag tac act cct gta tca tca aaa gcc atg tat 291
Val Lys Thr Tyr Gln Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr
80 85 90

gac gct tac tgg aac ggt aaa ttc aga gac tgc gct ttc cat tct ggc 339
Asp Ala Tyr Trp Asn Gly Lys Phe Arg Asp Cys Ala Phe His Ser Gly
95 100 105

ttt aat gag gat cca ttc gtt tgt gaa tat caa ggc caa tcg tct gac 387
Phe Asn Glu Asp Pro Phe Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp
110 115 120

ctg cct caa cct cct gtc aat gct tcc gga ggt ggt gga tcc 429
Leu Pro Gln Pro Pro Val Asn Ala Ser Gly Gly Gly Ser
125 130 135

gaggtgcagc tgctcgagcc cggtcaccgt ctcctcaggt ggtggtggtt ctggcgccgg 489

cggctccggc ggtggtggtt ctgagctcgg gacttagt 526

<210> 59

<211> 137

<212> PRT

<213> Artificial Sequence

<220>

<223> M13-Phage and artificial sequence of the MCS

<400> 59

Thr Lys Pro Pro Glu Tyr Gly Asp Thr Pro Ile Pro Gly Tyr Thr Tyr
1 5 10 15

Ile Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln Asn Pro
20 25 30

Ala Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn Thr Phe
35 40 45

Met Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu Thr Val
50 55 60

Tyr Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr Tyr Tyr
65 70 75 80

Gln Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr Trp Asn
85 90 95

Gly Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu Asp Pro
100 105 110

Phe Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro
115 120 125

Val Asn Ala Ser Gly Gly Gly Ser
130 135

<210> 60

<211> 726

<212> DNA

<213> Mus sp.

<220>

<221> CDS

<222> (1)..(726)

<223>

<400> 60

gag gtg cag ctg ctc gag cag tct gga gct gag ctg gtg aaa cct ggg
Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly
1 5 10 15

gcc tca gtg aag ata tcc tgc aag gct tct gga tac gcc ttc act aac

48

96

Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn			
20	25	30	
tac tgg cta ggt tgg gta aag cag agg cct gga cat gga ctt gag tgg			144
Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp			
35	40	45	
att gga gat ctt ttc cct gga agt ggt aat act cac tac aat gag agg			192
Ile Gly Asp Leu Phe Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg			
50	55	60	
ttc agg ggc aaa gcc aca ctg act gca gac aaa tcc tcg agc aca gcc			240
Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala			
65	70	75	80
ttt atg cag ctc agt agc ctg aca tct gag gac tct gct gtc tat ttc			288
Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe			
85	90	95	
tgt gca aga ttg agg aac tgg gac gag gct atg gac tac tgg ggc caa			336
Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln			
100	105	110	
ggg acc acg gtc acc gtc tcc tca ggt ggt ggt tct ggc ggc ggc			384
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly			
115	120	125	
ggc tcc ggt ggt ggt tct gag ctc gtc atg acc cag tct cca tct			432
Gly Ser Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser			
130	135	140	
tat ctt gct gca tct cct gga gaa acc att act att aat tgc agg gca			480
Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala			
145	150	155	160
agt aag agc att agc aaa tat tta gcc tgg tat caa gag aaa cct ggg			528
Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly			
165	170	175	
aaa act aat aag ctt ctt atc tac tct gga tcc act ttg caa tct gga			576
Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly			
180	185	190	
att cca tca agg ttc agt ggc agt gga tct ggt aca gat ttc act ctc			624
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu			
195	200	205	
acc atc agt agc ctg gag cct gaa gat ttt gca atg tat tac tgt caa			672
Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln			
210	215	220	
cag cat aat gaa tat ccg tac acg ttc gga ggg ggg acc aag ctt gag			720
Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu			
225	230	235	240
atc aaa			726
Ile Lys			

<210> 61
<211> 242
<212> PRT
<213> Mus sp.

<400> 61

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly
1 5 10 15

Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Leu Phe Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg
50 55 60

Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala
145 150 155 160

Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly
165 170 175

Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly
180 185 190

Ile	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu
195						200						205			

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln
210 215 220

Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
225 230 235 240

Ile Lys

<210> 62
<211> 753
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(753)
<223>

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<400> 62
gag gtg cag ctg ctc gag cag tct gga gct gag ctg gta agg cct ggg 48
Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1           5           10           15

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act tca gtg aag ctg tcc tgc aag gct tct ggc tac acc ttc aca agc 96
Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser
20          25          30

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tat ggt tta agc tgg gtg aag cag aga act gga cag ggc ctt gag tgg 144
 Tyr Gly Leu Ser Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp
 35 40 45

att gga gag gtt tat cct aga att ggt aat gct tac tac aat gag aag 192
 Ile Gly Val Tyr Pro Arg Ile Gly Asn Ala Tyr Tyr Asn Glu Lys
 50 55 60

ttc aag ggc aag gcc aca ctg act gca gac aaa tcc tcc agc aca gcg 240
 Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

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tcc atg gag ctc cgc agc ctg aca tct gag gac tct gcg gtc tat ttc 288
Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85          90          95
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tgt gca aga cgg gga tcc tac ggt agt aac tac gac tgg tac ttc gat 336
Cys Ala Arg Arg Gly Ser Tyr Gly Ser Asn Tyr Asp Trp Tyr Phe Asp
          100          105          110

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gtc tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt ggt ggt ggt		384	
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly			
115	120	125	
tct ggc ggc ggc tcc ggt ggt ggt tct gag ctc gtg atg acc		432	
Ser Gly Gly Gly Ser Gly Gly Ser Gly Ser Glu Leu Val Met Thr			
130	135	140	
cag act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc		480	
Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile			
145	150	155	160
tct tgc aga tct agt cag agc ctt gta cac agt aat gga aac acc tat		528	
Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr			
165	170	175	
tta cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc		576	
Leu His Trp Tyr Leu Gln Lys Pro Gly Gin Ser Pro Lys Leu Leu Ile			
180	185	190	
tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc		624	
Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly			
195	200	205	
agt gga tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct		672	
Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala			
210	215	220	
gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac		720	
Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr			
225	230	235	240
acg ttc gga ggg ggg acc aag ctt gag atc aaa		753	
Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys			
245	250		
<210> 63			
<211> 251			
<212> PRT			
<213> Mus sp.			
<400> 63			
Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly			
1	5	10	15
Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser			
20	25	30	
Tyr Gly Leu Ser Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp			
35	40	45	
Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr Tyr Asn Glu Lys			

50

55

60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Arg Gly Ser Tyr Gly Ser Asn Tyr Asp Trp Tyr Phe Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Leu Val Met Thr
130 135 140

Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile
145 150 155 160

Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr
165 170 175

Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
180 185 190

Tyr Lys Val¹ Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
210 215 220

Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr
225 230 235 240

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
245 250

<210> 64
<211> 726
<212> DNA
<213> Mus sp.

<220>

<221> CDS
<222> (1)..(726)
<223>

<400> 64
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Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Ala Leu Val Arg Pro Gly
1 5 10 15
act tca gtg aag ata tcc tgc aag gct tct gga tac gcc ttc act aac 96
Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30
tac tgg cta ggt tgg gta aag cag agg cct gga cat gga ctt gag tgg 144
Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45
att gga gat att tac cct gga agt ggt aat act cac tac aat gag agg 192
Ile Gly Asp Ile Tyr Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg
50 55 60
ttc agg ggc aaa gcc aca ctg act gca gac aaa tcc tcg agc aca gcc 240
Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80
ttt atg cag ctc agt agc ctg aca tct gag gac tct gct gtc tat ttc 288
Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95
tgt gca aga ttg agg aac tgg gac gag cct atg gac tac tgg ggc caa 336
Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
100 105 110
ggg acc acg gtc acc gtc tcc tca ggt ggt ggt tct ggc ggc ggc 384
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
115 120 125
ggc tcc ggt ggt ggt tct gag ctc cag atg acc cag tct cca tct 432
Gly Ser Gly Gly Ser Glu Leu Gln Met Thr Gln Ser Pro Ser
130 135 140
tat ctt gct gca tct cct gga gaa acc att act att aat tgc agg gca 480
Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala
145 150 155 160
agt aag agc att agc aaa tat tta gcc tgg tat caa gag aaa cct ggg 528
Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly
165 170 175
aaa act aat aag ctt ctt atc tac tct gga tcc act ttg caa tct gga 576
Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly
180 185 190
att cca tca agg ttc agt ggc agt gga tct ggt aca gat ttc act ctc 624
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

acc atc agt agc ctg gag cct gaa gat ttt gca atg tat tac tgt caa	672														
Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln															
210	215	220		cag cat aat gaa tac ccg tac acg ttc gga ggg ggg acc aag ctt gag	720	Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu		225	230	235	240	atc aaa	726	Ile Lys	
220															
cag cat aat gaa tac ccg tac acg ttc gga ggg ggg acc aag ctt gag	720														
Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu															
225	230	235	240	atc aaa	726	Ile Lys									
235	240														
atc aaa	726														
Ile Lys															

<210> 65
<211> 242
<212> PRT
<213> Mus sp.

<400> 65

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Ala Leu Val Arg Pro Gly			
1	5	10	15
10	15		

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn			
20	25	30	
30			

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp			
35	40	45	
45			

Ile Gly Asp Ile Tyr Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg			
50	55	60	
60			

Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala			
65	70	75	80
75	80		

Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe			
85	90	95	
95			

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln			
100	105	110	
110			

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly			
115	120	125	
125			

Gly Ser Gly Gly Gly Ser Glu Leu Gln Met Thr Gln Ser Pro Ser			
130	135	140	
140			

Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala
145 150 155 160

Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly
165 170 175

Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly
180 185 190

Ile Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln
210 215 220

Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu
225 230 235 240

Ile Lys

<210> 66
<211> 744
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(744)
<223>

<400> 66
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Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

act tca gtg aag ata tcc tgc aag gct tct gga tac gcc ttc act aac 96
Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

tac tgg cta ggt tgg gtt aag cag agg cct gga cat gga ctt gaa tgg 144
Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

gtt gga gat att ttc cct gga agt ggt aat gct cac tac aat gag aag 192
Val Gly Asp Ile Phe Pro Gly Ser Gly Asn Ala His Tyr Asn Glu Lys
50 55 60

ttc aag ggc aaa gcc aca ctg act gca gac aag tcc tcg tac aca gcc 240

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Tyr Thr Ala				
65	70	75	80	
tat atg cag ctc agt agc ctg aca tct gag gac tct gct gtc tat ttc				288
Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe				
85	90	95		
tgt gca aga ttg cgg aac tgg gac gag gct atg gac tac tgg ggc caa				336
Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln				
100	105	110		
ggg acc acg gtc acc gtc tcc tca ggt ggt ggt tct ggc ggc ggc				384
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly				
115	120	125		
ggc tcc ggt ggt ggt tct gag ctc gtg atg aca cag tct cca tcc				432
Gly Ser Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser				
130	135	140		
tcc ctg agt gtg tca gca gga gag aag gtc act atg agc tgc aag tcc				480
Ser Leu Ser Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser				
145	150	155	160	
agt cag agt ctg tta aac agt gga aat caa aag aac tac ttg gcc tgg				528
Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp				
165	170	175		
tac cag cag aaa cca ggg cag cct cct aaa ctg ttg atc tac ggg gca				576
Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gly Ala				
180	185	190		
tcc act agg gaa tct ggg gtc cct gat cgc ttc aca ggc agt gga tct				624
Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser				
195	200	205		
gga aca gat ttc act ctc acc atc agc agt gtg cag gct gaa gac ctg				672
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu				
210	215	220		
gca gtt tat tac tgt cag aat gat tat agt tat ccg tac acg ttc gga				720
Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly				
225	230	235	240	
ggg ggg acc aag ctt gag atc aaa				744
Gly Gly Thr Lys Leu Glu Ile Lys				
245				

<210> 67
 <211> 248
 <212> PRT
 <213> Mus sp.

<400> 67

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly				
1	5	10	15	

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Val Gly Asp Ile Phe Pro Gly Ser Gly Asn Ala His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Tyr Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Ser Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gly Ala
180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly
225 230 235 240

Gly Gly Thr Lys Leu Glu Ile Lys
245

<210> 68
<211> 726
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(726)
<223>

<400> 68
gag gtg cag ctg ctc gag cag tct gga gct gag ctg gtg agg cct ggg 48
Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15
gct tca gtg aag ata tcc tgc aag gct tct gga tac gcc ttc aat aac 96
Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Asn Asn
20 25 30
tac tgg cta ggt tgg gta aag cag agg cct gga cat gga ctt gag tgg 144
Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45
att gga gac att tac cct gga agt gga aat act cac tac aat gag agg 192
Ile Gly Asp Ile Tyr Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg
50 55 60
ttc agg ggc aaa gcc aca ctg act gca gac aaa tcc tcg agc aca gcc 240
Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80
ttt atg cag tta agt agc ctg aca tct gag gac tct gct gtc tat ttc 288
Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95
tgt gca aga ttg agg aac tgg gac gag gct atg gac tac tgg ggc caa 336
Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln
100 105 110
ggg acc acg gtc acc gtc tcc tca ggt ggt ggt tct ggc ggc ggc 384
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
115 120 125
ggc tcc ggt ggt ggt tct gag ctc gtc atg acc cag tct cca tct 432
Gly Ser Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140
tat ctt gct gca tct cct gga gaa acc att act att aat tgc agg gca 480
Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala
145 150 155 160

agt aag agc att agc aaa tat tta gcc tgg tat caa gag aaa cct ggg	528																																								
Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly																																									
165	170		175	aaa act aat aag ctt ctt atc tac tct gga tcc act ttg caa tct gga	576	Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly		180	185		190	att cca tca agg ttc agt ggc agt gga tct ggt aca gat ttc act ctc	624	Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu		195	200		205	acc atc agt agc ctg gag cct gaa gat ttt gca atg tat tac tgt caa	672	Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln		210	215		220	cag cat aat gaa tac ccg tac acg ttc gga ggg ggg acc aag ctt gag	720	Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu		225	230		235		240	atc aaa	726	Ile Lys	
	175																																								
aaa act aat aag ctt ctt atc tac tct gga tcc act ttg caa tct gga	576																																								
Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly																																									
180	185		190	att cca tca agg ttc agt ggc agt gga tct ggt aca gat ttc act ctc	624	Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu		195	200		205	acc atc agt agc ctg gag cct gaa gat ttt gca atg tat tac tgt caa	672	Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln		210	215		220	cag cat aat gaa tac ccg tac acg ttc gga ggg ggg acc aag ctt gag	720	Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu		225	230		235		240	atc aaa	726	Ile Lys									
	190																																								
att cca tca agg ttc agt ggc agt gga tct ggt aca gat ttc act ctc	624																																								
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu																																									
195	200		205	acc atc agt agc ctg gag cct gaa gat ttt gca atg tat tac tgt caa	672	Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln		210	215		220	cag cat aat gaa tac ccg tac acg ttc gga ggg ggg acc aag ctt gag	720	Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu		225	230		235		240	atc aaa	726	Ile Lys																	
	205																																								
acc atc agt agc ctg gag cct gaa gat ttt gca atg tat tac tgt caa	672																																								
Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln																																									
210	215		220	cag cat aat gaa tac ccg tac acg ttc gga ggg ggg acc aag ctt gag	720	Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu		225	230		235		240	atc aaa	726	Ile Lys																									
	220																																								
cag cat aat gaa tac ccg tac acg ttc gga ggg ggg acc aag ctt gag	720																																								
Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu																																									
225	230		235		240	atc aaa	726	Ile Lys																																	
	235		240	atc aaa	726	Ile Lys																																			
	240																																								
atc aaa	726																																								
Ile Lys																																									

<210> 69
 <211> 242
 <212> PRT
 <213> Mus sp.

<400> 69

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly					
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	10				
	15				

Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Asn Asn			
20	25		30
	30		

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp			
35	40		45
	45		

Ile Gly Asp Ile Tyr Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg			
50	55		60
	60		

Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala					
65	70		75		80
	75		80		
	80				

Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe			
85	90		95
	95		

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala
145 150 155 160

Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly
165 170 175

Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly
180 185 190

Ile Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln
210 215 220

Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu
225 230 235 240

Ile Lys

<210> 70

<211> 753

<212> DNA

<213> Mus sp.

<220>

<221> CDS

<222> (1)...(753)

<223>

<400> 70

gag gtg cag ctg ctc gag cag tct gga gct gag ctg gcg agg cct ggg
Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly
1 5 10 15

gct tca gtg aag ctg tcc tgc aag gct tct ggc tac acc ttc aca aac
Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn

48

96

20

25

30

tat ggt tta agc tgg gtg aag cag agg cct gga cag gtc ctt gag tgg	144		
Tyr Gly Leu Ser Trp Val Lys Gln Arg Pro Gly Gln Val Leu Glu Trp			
35	40	45	
att gga gag gtt tat cct aga att ggt aat gct tac tac aat gag aag	192		
Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr Tyr Asn Glu Lys			
50	55	60	
ttc aag ggc aag gcc aca ctg act gca gac aaa tcc tcc agc aca gcg	240		
Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala			
65	70	75	80
tcc atg gag ctc cgc agc ctg acc tct gag gac tct gcg gtc tat ttc	288		
Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe			
85	90	95	.
tgt gca aga cgg gga tcc tac gat act aac tac gac tgg tac ttc gat	336		
Cys Ala Arg Arg Gly Ser Tyr Asp Thr Asn Tyr Asp Trp Tyr Phe Asp			
100	105	110	
gtc tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt ggt ggt ggt	384		
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly			
115	120	125	
tct ggc ggc ggc tcc ggt ggt ggt ggt tct gag ctc gtg atg acc	432		
Ser Gly Gly Gly Ser Gly Gly Ser Gly Ser Glu Leu Val Met Thr			
130	135	140	
cag act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc	480		
Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile			
145	150	155	160
tct tgc aga tct agt cag agc ctt gta cac agt aat gga aac acc tat	528		
Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr			
165	170	175	
tta cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc	576		
Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile			
180	185	190	
tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc	624		
Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly			
195	200	205	
agt gga tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct	672		
Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala			
210	215	220	
gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac	720		
Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr			
225	230	235	240
acg ttc gga ggg acc aag ctt gag atc aaa	753		
Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys			
245	250		

<210> 71
<211> 251
<212> PRT
<213> Mus sp.

<400> 71

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly
1 5 10 15

Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn
20 25 30

Tyr Gly Leu Ser Trp Val Lys Gln Arg Pro Gly Gln Val Leu Glu Trp
35 40 45

Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Arg Gly Ser Tyr Asp Thr Asn Tyr Asp Trp Tyr Phe Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Ser Gly Gly Gly Ser Gly Gly Ser Glu Leu Val Met Thr
130 135 140

Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile
145 150 155 160

Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr
165 170 175

Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
180 185 190

Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
210 215 220

Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr
225 230 235 240

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
245 250

<210> 72
<211> 717
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(717)
<223>

<400> 72
gag gtg cag ctg ctc gag tct gga ggt ggc ctg gtg cag cct gga gga 48
Glu Val Gln Leu Leu Ser Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

tcc ctg aaa ctc tcc tgt gca gcc tca gga ttc gat ttt agt aga tac 96
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr
20 25 30

tgg atg agt tgg gtc cgg cag gct cca ggg aaa ggg cta gaa tgg att 144
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

gga gaa att aat cca gat agc agt acg ata aac tat acg cca tct ctg 192
Gly Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Ser Leu
50 55 60

aag gat aaa ttc atc atc tcc aga gac aac gcc aaa aat acg ctg tac 240
Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

ctg caa atg ggc aaa gtg aga tct gag gac aca gcc ctt tat tac tgt 288
Leu Gln Met Gly Lys Val Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

gca aga gga gcc ttc ctt ttt gac tac tgg ggc caa ggg acc acg gtc 336
Ala Arg Gly Ala Phe Leu Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

acc gtc tcc tca ggt ggt ggt tct ggc ggc ggc tcc ggt ggt 384

Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly			
115	120	125	
ggt ggt tct gag ctc gtg ctc acc cag tct cca acc acc atg gct gca			432
Gly Gly Ser Glu Leu Val Leu Thr Gln Ser Pro Thr Thr Met Ala Ala			
130	135	140	
tct ccc ggg gag aag atc act atc acc tgc agt gcc agc tca agt ata			480
Ser Pro Gly Glu Lys Ile Thr Ile Thr Cys Ser Ala Ser Ser Ser Ile			
145	150	155	160
agt tcc aat tac ttg cat tgg tat cag cag aag cca gga ttc tcc cct			528
Ser Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Phe Ser Pro			
165	170	175	
aaa ctc ttg att tat agg aca tcc aat ctg gct tct gga gtc cca gct			576
Lys Leu Leu Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ala			
180	185	190	
cgc ttc agt ggc agt ggg tct ggg acc tct tac tct ctc aca att ggc			624
Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Gly			
195	200	205	
acc atg gag gct gaa gat gtt gcc act tac tac tgc cag cag ggt agt			672
Thr Met Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Gly Ser			
210	215	220	
agt ata cca ctc acg ttc ggt gct ggg acc aag ctt gag atc aaa			717
Ser Ile Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys			
225	230	235	

<210> 73
 <211> 239
 <212> PRT
 <213> Mus sp.

 <400> 73

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr
 20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Gly Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Ser Leu
 50 55 60

Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Gly Lys Val Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Arg Gly Ala Phe Leu Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Glu Leu Val Leu Thr Gln Ser Pro Thr Thr Met Ala Ala
130 135 140

Ser Pro Gly Glu Lys Ile Thr Ile Thr Cys Ser Ala Ser Ser Ser Ile
145 150 155 160

Ser Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Phe Ser Pro
165 170 175

Lys Leu Leu Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ala
180 185 190

Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Gly
195 200 205

Thr Met Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Gly Ser
210 215 220

Ser Ile Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys
225 230 235

<210> 74
<211> 744
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(744)
<223>

<400> 74
gag gtg cag ctg ctc gag cag tct gga gct gag ctg gta agg cct ggg
Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

48

act tca gtg aag ata tcc tgc aag gct tct gga tac gcc ttc act aac	96
Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn	
20 25 30	
tac tgg cta ggt tgg gta aag cag agg cct gga cat gga ctt gag tgg	144
Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp	
35 40 45	
att gga gat att ttc cct gga agt ggt aat atc cac tac aat gag aag	192
Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys	
50 55 60	
ttc aag ggc aaa gcc aca ctg act gca gac aaa tct tcg agc aca gcc	240
Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala	
65 70 75 80	
tat atg cag ctc agt agc ctg aca ttt gag gac tct gct gtc tat ttc	288
Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe	
85 90 95	
tgt gca aga ctg agg aac tgg gac gag cct atg gac tac tgg ggc caa	336
Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln	
100 105 110	
ggg acc acg gtc acc gtc tcc tca ggt ggt ggt tct ggc ggc ggc	384
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly	
115 120 125	
ggc tcc ggt ggt ggt tct gag ctc gtg atg aca cag tct cca tcc	432
Gly Ser Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser	
130 135 140	
tcc ctg act gtg aca gca gga gag aag gtc act atg agc tgc aag tcc	480
Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser	
145 150 155 160	
agt cag agt ctg tta aac agt gga aat caa aag aac tac ttg acc tgg	528
Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp	
165 170 175	
tac cag cag aaa cca ggg cag cct cct aaa ctg ttg atc tac tgg gca	576
Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala	
180 185 190	
tcc act agg gaa tct ggg gtc cct gat cgc ttc aca ggc agt gga tct	624
Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser	
195 200 205	
gga aca gat ttc act ctc acc atc agc agt gtg cag gct gaa gac ctg	672
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu	
210 215 220	
gca gtt tat tac tgt cag aat gat tat agt tat ccg ctc acg ttc ggt	720
Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly	
225 230 235 240	

gct ggg acc aag ctt gag atc aaa
Ala Gly Thr Lys Leu Glu Ile Lys
245

744

<210> 75
<211> 248
<212> PRT
<213> Mus sp.

<400> 75

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala

180

185

190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
 210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
 225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys
 245

<210> 76
 <211> 744
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (1)...(744)
 <223>

<400> 76
 gag gtg cag ctg ctc gag cag tct gga gct gag ctg gta agg cct ggg 48
 Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 1 5 10 15
 act tca gtg aag ata tcc tgc aag gct tct gga tac gcc ttc act aac 96
 Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 20 25 30
 tac tgg cta ggt tgg gtt aag cag agg cct gga cat gga ctt gaa tgg 144
 Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 35 40 45
 gtt gga gat att ttc cct gga agt aat gct cac tac aat gag aag 192
 Val Gly Asp Ile Phe Pro Gly Ser Gly Asn Ala His Tyr Asn Glu Lys
 50 55 60
 ttc aag ggc aaa gcc aca ctg act gca gac aag tcc tcg tac aca gcc 240
 Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Tyr Thr Ala
 65 70 75 80
 tat atg cag ctc agt agc ctg aca tct gag gac tct gct gtc tat ttc 288
 Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
 85 90 95
 tgt gca aga ttg cgg aac tgg gac gag gct atg gac tac tgg ggc caa 336
 Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln

100	105	110	
ggg acc acg gtc acc gtc tcc tca ggt ggt ggt ggt tct ggc ggc Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly			384
115	120	125	
ggc tcc ggt ggt ggt tct gag ctc gtg atg aca cag tct cca tcc Gly Ser Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser			432
130	135	140	
tcc ctg gct atg tca gta gga cag aag gtc act atg agc tgc aag tcc Ser Leu Ala Met Ser Val Gly Gln Lys Val Thr Met Ser Cys Lys Ser			480
145	150	155	160
agt cag agc ctt tta aat agt agc aat caa aag aac tat ttg gcc tgg Ser Gln Ser Leu Leu Asn Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp			528
165	170	175	
tac cag cag aaa caa ggg cag cct cct aaa ctg ctt atc tat ggg gca Tyr Gln Gln Lys Gln Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gly Ala			576
180	185	190	
tcc att aga gaa tct tgg gtc cct gat cga ttc aca gga agt gga tct Ser Ile Arg Glu Ser Trp Val Pro Asp Arg Phe Thr Gly Ser Gly Ser			624
195	200	205	
ggg aca gac ttc act ctc acc atc agc agt gtg aag gct gaa gac ctg Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Lys Ala Glu Asp Leu			672
210	215	220	
gca gtt tat tac tgt cag caa tat tat agc tat ccg tac acg ttc gga Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Tyr Thr Phe Gly			720
225	230	235	240
ggg ggg acc aag ctt gag atc aaa Gly Gly Thr Lys Leu Glu Ile Lys			744
245			

<210> 77
 <211> 248
 <212> PRT
 <213> Mus sp.

<400> 77

Glu	Val	Gln	Leu	Leu	Glu	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly
1				5			10						15		

Thr	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe	Thr	Asn
				20			25					30			

Tyr	Trp	Leu	Gly	Trp	Val	Lys	Gln	Arg	Pro	Gly	His	Gly	Leu	Glu	Trp
						35		40			45				

Val Gly Asp Ile Phe Pro Gly Ser Gly Asn Ala His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Tyr Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Ala Met Ser Val Gly Gln Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp
165 170 175

Tyr Gln Gln Lys Gln Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gly Ala
180 185 190

Ser Ile Arg Glu Ser Trp Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Lys Ala Glu Asp Leu
210 215 220

Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Tyr Thr Phe Gly
225 230 235 240

Gly Gly Thr Lys Leu Glu Ile Lys
245